

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2001, 16:51:40 ; Search time 45.66 Seconds

(Without alignments)  
2159.167 Million cell updates/sec

Title: US-09-830-647-1

Perfect score: 3510  
Sequence: 1 MNSGAMRIIRSKGHFGGIGV.....SDNLIRAFSPSPSTFTTGP 674

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_17:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp rodent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3510	100.0	674	4 Q9UBU7	Q9ubut homo sapien
2	3124	89.0	601	4 O75226	O75226 homo sapien
3	2483	70.7	676	11 Q99WU0	Q99WU0 cricetus
4	2240.5	63.8	663	11 Q9QZ41	Q9qz41 mus musculu
5	1303.5	37.1	321	11 Q9CXP2	Q9cxf2 mus musculu
6	1170	33.3	234	4 Q9YZM6	Q9yzm6 homo sapien
7	1170	7.8	1695	5 Q9UR85	Q9ur85 drosophila
8	273	7.8	1695	5 Q9NK53	Q9nk53 drosophila
9	273	7.8	1711	5 Q9VJL0	Q9vj10 drosophila
10	273	7.8	1711	5 Q9UR94	Q9ur94 drosophila
11	208	5.9	170	4 Q9H912	Q9h912 homo sapien
12	187	5.3	1790	3 Q07380	Q07380 saccharomyc
13	182	5.2	1173	2 Q9AHK6	Q9ahk6 borrelia bu
14	181.5	5.2	1578	10 Q9AV25	Q9av25 oryza sativ
15	177	5.0	1344	2 Q49545	Q49545 mycoplasma
16	175	5.0	1084	4 Q9NXG0	Q9nxc0 homo sapien
17	173	4.9	1365	2 Q49525	Q49525 mycoplasma
18	170.5	4.9	911	3 Q06704	Q06704 saccharomyc
19	170	4.8	1388	4 Q9NS87	Q9ns87 homo sapien

20	170	4.8	1516	5 Q96154	Q96154 plasmodium
21	168	4.8	1065	2 Q9AHK9	Q9ahk9 borrelia bu
22	168	4.8	1065	2 Q9AHK8	Q9ahk8 borrelia bu
23	166.5	4.7	1871	10 Q9SRD5	Q9srd5 arabidopsis
24	166	4.7	1330	6 Q97961	Q97961 vulpes vulp
25	165	4.7	849	2 Q9AHK4	Q9ahk4 borrelia bu
26	165	4.7	1119	2 Q51228	Q51228 borrelia bu
27	164.5	4.7	2062	4 Q9H231	Q9h231 homo sapien
28	164	4.7	646	5 Q96147	Q96147 plasmodium
29	164	4.7	1946	5 Q97291	Q97291 plasmodium
30	163.5	4.7	2771	5 Q26216	Q26216 plasmodium
31	163	4.6	1278	4 Q9UPP5	Q9upp5 homo sapien
32	162	4.6	1583	4 Q15045	Q15045 homo sapien
33	162	4.6	2269	5 Q26223	Q26223 plasmodium
34	161.5	4.6	1179	2 Q9AHK3	Q9ahk3 borrelia bu
35	161	4.6	957	2 Q9AH11	Q9ah11 borrelia bu
36	161	4.6	1300	4 Q13999	Q13999 homo sapien
37	161	4.6	1356	4 Q14707	Q14707 homo sapien
38	161	4.6	2205	5 Q9NG02	Q9ng02 dictyostell
39	161	4.6	6815	5 Q91704	Q91704 drosophila
40	158.5	4.5	1978	4 Q15154	Q15154 homo sapien
41	158.5	4.5	1979	4 Q95949	Q95949 homo sapien
42	158	4.5	891	4 Q9Y2K3	Q9y2k3 homo sapien
43	158	4.5	980	5 Q96246	Q96246 plasmodium
44	158	4.5	1271	5 Q25860	Q25860 plasmodium
45	158	4.5	3124	5 Q9GYB8	Q9gyb8 plasmodium

## ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	674 AA.
Q9UBU7	Q9UBU7	Q9UBU7		
AC	Q9UBU7	Q9UBU7		
ID	Q9UBU7	Q9UBU7		
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	ACTIVATOR OF S PHASE KINASE.			
GN	ASK/H37 OR DBF4.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kumagai H., Sato N., Yamada M., Mahony D., Seghezzi W., Lees E.,			
RA	Arai K., Masai H.;			
RT	"A Novel Growth- and Cell Cycle-Regulated Protein, ASK, Activates			
RT	Human Cdc7-Related Kinase and Is Essential for G1/S transition in			
RT	Mammalian Cells.";			
RL	Mol. Cell. Biol. 0:0-0(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Jiang W., Hunter T.;			
RT	"Mammalian Cdc7/Dbp4 Protein Kinase Complex is Essential for			
RT	Initiation of DNA Replication.";			
RL	Submitted (Jun-1999) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Hollingsworth R.;			
RT	"Use of a semi-automated yeast two-hybrid system to identify proteins			
RT	that interact with the human Cdc7 protein.";			
RL	Submitted (Jun-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB028069; BAA78326.1; -			
DR	EMBL; AF160249; AAD41911.1; -			
DR	EMBL; AF160876; AAD45357.1; -			
DR	InterPro; IPR001357; BRCT.			
DR	SMART; SM00292; BRCT; 1.			
SQ	SEQUENCE 674 AA; 76857 MW; 353FEB7E85507E5C CRC64;			

Query Match 100.0%; Score 3510; DB 4; Length 674;



RL Gene 264:249-256(2001).  
 DR EMBL: AF292400; AAK21856.1; -  
 SQ SEQUENCE 676 AA; 75849 MW; EC7EEBDD80D40B8C CRC64;

Query Match 70.7%; Score 2483; DB 11; Length 676;  
 Best Local Similarity 71.6%; Pred. No. 2,8e-151;  
 Matches 488; Conservative 82; Mismatches 98; Indels 14; Gaps 7;

```

QY 1 MNSGAMRIHSGHFGGQIQVQKNEKNRPSLSKLTQDNREPKSKCKPLMGKVFYLDLPSTVI 60
DB 1 MNSGAMRIHSGHFGGQIQVQKNEKNRPSLSKLTQDNREPKSKCKPLMGKVFYLDLPSTVI 60
QY 61 SEKLODKIDJGGRVEEFLSKDISYLSNKKKAKFAQTIGRISPVSPSASATTAETTSPI 120
DB 61 SEKLODKIDJGGRVEEFLSKDISYLSNKKKAKFAQTIGRISPVSPSASATTAETTSPI 120
QY 121 PSHDSSFFKSPDYVCLSRGKLLVEKAIKDHPFIPNSILSNLSMGVKILHIDIRYIE 180
DB 121 PSHDSSFFKSPDYVCLSRGKLLVEKAIKDHPFIPNSILSNLSMGVKILHIDIRYIE 180
QY 121 PSHDSSFFKSPDYVCLSRGKLLVEKAIKDHPFIPNSILSNLSMGVKILHIDIRYIE 180
DB 121 PSHDSSFFKSPDYVCLSRGKLLVEKAIKDHPFIPNSILSNLSMGVKILHIDIRYIE 180
QY 181 OKKKELYLLKSSSVYRDGKRVSGAOKTGTGLKPKFVKVEDMSQLYRPYLOLTNMP 240
DB 181 OKKKELYLLKSSSVYRDGKRVSGAOKTGTGLKPKFVKVEDMSQLYRPYLOLTNMP 240
QY 241 FINYSIOKPCSPFDVDRKSSMOKOTQVARIQTOGDKYGGTSIOLEKPKKKGYCECCL 300
DB 241 FINYSIOKPCSPFDVDRKSSMOKOTQVARIQTOGDKYGGTSIOLEKPKKKGYCECCL 300
QY 301 OKYEDLETHLLSEOHNRNFAOSNOQVVDIVSKLVDFEVEYEKDPKKRIKYSVGLSP 360
DB 301 OKYEDLETHLLSEOHNRNFAOSNOQVVDIVSKLVDFEVEYEKDPKKRIKYSVGLSP 360
QY 301 OKYEDLETHLLSEOHNRNFAOSNOQVVDIVSKLVDFEVEYEKDPKKRIKYSVGLSP 360
DB 301 OKYEDLETHLLSEOHNRNFAOSNOQVVDIVSKLVDFEVEYEKDPKKRIKYSVGLSP 360
QY 361 VSASYLKTQEKKEVELQHSQKDCQEDDTVKEQNF----LYKETQETEKLLFTISEP 415
DB 361 VSASYLKTQEKKEVELQHSQKDCQEDDTVKEQNF----LYKETQETEKLLFTISEP 415
QY 416 IPHNSNEIRGLNEKSNKSMSTAEEDIRQNTQOLPIHKKKQCECILDISETL--SEMD 473
DB 416 IPHNSNEIRGLNEKSNKSMSTAEEDIRQNTQOLPIHKKKQCECILDISETL--SEMD 473
QY 421 MYSYTGKLGKDEKAA--SMINASEPIDIKQFTQLPPCKMEQEGILVSEKLLINRND 477
DB 421 MYSYTGKLGKDEKAA--SMINASEPIDIKQFTQLPPCKMEQEGILVSEKLLINRND 477
QY 474 LEEILRVADHYKCNIAQSVHSPDSTNSGQPKQSDVYLPFAKDLKEKDLHSIFTHDSGL 533
DB 474 LEEILRVADHYKCNIAQSVHSPDSTNSGQPKQSDVYLPFAKDLKEKDLHSIFTHDSGL 533
QY 478 LEO-RVGCSSVQVPSGVSHLSPENSLPQPKLADTHHSKADLOEKDOLHVPFHDSDL 536
DB 478 LEO-RVGCSSVQVPSGVSHLSPENSLPQPKLADTHHSKADLOEKDOLHVPFHDSDL 536
QY 534 ITINSSQEHLLVOAKAPHTPPEEPNECDFFKNMDSLPSGKIHRRYKAILGRNRKKNLEPN 593
DB 534 ITINSSQEHLLVOAKAPHTPPEEPNECDFFKNMDSLPSGKIHRRYKAILGRNRKKNLEPN 593
QY 537 VTLNMSKEQLIVYKAGTP--SCGPQGNEDCTENTDNLPGCKIQRKVRLLDGO-KKKNVDP 594
DB 537 VTLNMSKEQLIVYKAGTP--SCGPQGNEDCTENTDNLPGCKIQRKVRLLDGO-KKKNVDP 594
QY 594 AEPD-KRTEPTTQEBNRICSSPVOSLLDLFQTSSEKSEFLGFTSTYKSGICNVLDIWE 652
DB 594 AEPD-KRTEPTTQEBNRICSSPVOSLLDLFQTSSEKSEFLGFTSTYKSGICNVLDIWE 652
QY 653 ENSDNLTAFFSSPSTSTGTG 674
DB 653 ENSDNLTAFFSSPSTSTGTG 674
QY 655 ENSSSLSTFFSSPSASTGTG 676
DB 655 ENSSSLSTFFSSPSASTGTG 676

```

RESULT 4

090241 PRELIMINARY; PRT; 663 AA.  
 AC 090241;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE DHR4-RELATED PROTEIN.  
 GN ASK OR MUDBF4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=99444905; PubMed=10517317;  
 RA Lepke M., Puettler V., Stalib C., Kneissl M., Berger C., Hoehn K.,  
 RA Nanda I., Schmid M., Grubert F.;  
 RT "Identification, characterization and chromosomal localization of the  
 RT cognate human and murine Dhr4 genes.";  
 RL Mol. Gen. Genet. 262:220-229(1999).  
 DR EMBL: AJ003132; CAB56847.1; -  
 DR MGD: MGI:1351328; Ask.  
 SQ SEQUENCE 663 AA; 74175 MW; 72E05CB87C3B1650 CRC64;

Query Match 63.8%; Score 2240.5; DB 11; Length 663;  
 Best Local Similarity 66.6%; Pred. No. 9.4e-136;  
 Matches 451; Conservative 76; Mismatches 133; Indels 17; Gaps 8;

```

QY 1 MNSGAMRIHSGHFGGQIQVQKNEKNRPSLSKLTQDNREPKSKCKPLMGKVFYLDLPSTVI 60
DB 1 MNSGAMRIHSGHFGGQIQVQKNEKNRPSLSKLTQDNREPKSKCKPLMGKVFYLDLPSTVI 60
QY 61 SEKLODKIDJGGRVEEFLSKDISYLSNKKKAKFAQTIGRISPVSPSASATTAETTSPI 120
DB 61 SEKLODKIDJGGRVEEFLSKDISYLSNKKKAKFAQTIGRISPVSPSASATTAETTSPI 120
QY 121 PSHDSSFFKSPDYVCLSRGKLLVEKAIKDHPFIPNSILSNLSMGVKILHIDIRYIE 180
DB 121 PSHDSSFFKSPDYVCLSRGKLLVEKAIKDHPFIPNSILSNLSMGVKILHIDIRYIE 180
QY 121 PSHDSSFFKSPDYVCLSRGKLLVEKAIKDHPFIPNSILSNLSMGVKILHIDIRYIE 180
DB 121 PSHDSSFFKSPDYVCLSRGKLLVEKAIKDHPFIPNSILSNLSMGVKILHIDIRYIE 180
QY 181 OKKKELYLLKSSSVYRDGKRVSGAOKTGTGLKPKFVKVEDMSQLYRPYLOLTNMP 240
DB 181 OKKKELYLLKSSSVYRDGKRVSGAOKTGTGLKPKFVKVEDMSQLYRPYLOLTNMP 240
QY 241 FINYSIOKPCSPFDVDRKSSMOKOTQVARIQTOGDKYGGTSIOLEKPKKKGYCECCL 300
DB 241 FINYSIOKPCSPFDVDRKSSMOKOTQVARIQTOGDKYGGTSIOLEKPKKKGYCECCL 300
QY 301 OKYEDLETHLLSEOHNRNFAOSNOQVVDIVSKLVDFEVEYEKDPKKRIKYSVGLSP 360
DB 301 OKYEDLETHLLSEOHNRNFAOSNOQVVDIVSKLVDFEVEYEKDPKKRIKYSVGLSP 360
QY 301 OKYEDLETHLLSEOHNRNFAOSNOQVVDIVSKLVDFEVEYEKDPKKRIKYSVGLSP 360
DB 301 OKYEDLETHLLSEOHNRNFAOSNOQVVDIVSKLVDFEVEYEKDPKKRIKYSVGLSP 360
QY 361 VSASYLKTQEKKEVELQHSQKDCQEDDTVKEQNF----LYKETQETEKLLFTISEP 415
DB 361 VSASYLKTQEKKEVELQHSQKDCQEDDTVKEQNF----LYKETQETEKLLFTISEP 415
QY 416 IPHNSNEIRGLNEKSNKSMSTAEEDIRQNTQOLPIHKKKQCECILDISETL--SEMD 473
DB 416 IPHNSNEIRGLNEKSNKSMSTAEEDIRQNTQOLPIHKKKQCECILDISETL--SEMD 473
QY 421 MYSYTGKLGKDEKAA--SMINASEPIDIKQFTQLPPCKMEQEGILVSEKLLINRND 477
DB 421 MYSYTGKLGKDEKAA--SMINASEPIDIKQFTQLPPCKMEQEGILVSEKLLINRND 477
QY 474 LEEILRVADHYKCNIAQSVHSPDSTNSGQPKQSDVYLPFAKDLKEKDLHSIFTHDSGL 533
DB 474 LEEILRVADHYKCNIAQSVHSPDSTNSGQPKQSDVYLPFAKDLKEKDLHSIFTHDSGL 533
QY 478 LEO-RVGCSSVQVPSGVSHLSPENSLPQPKLADTHHSKADLOEKDOLHVPFHDSDL 536
DB 478 LEO-RVGCSSVQVPSGVSHLSPENSLPQPKLADTHHSKADLOEKDOLHVPFHDSDL 536
QY 534 ITINSSQEHLLVOAKAPHTPPEEPNECDFFKNMDSLPSGKIHRRYKAILGRNRKKNLEPN 593
DB 534 ITINSSQEHLLVOAKAPHTPPEEPNECDFFKNMDSLPSGKIHRRYKAILGRNRKKNLEPN 593
QY 537 VTLNMSKEQLIVYKAGTP--SCGPQGNEDCTENTDNLPGCKIQRKVRLLDGO-QANNEPSELDK 594
DB 537 VTLNMSKEQLIVYKAGTP--SCGPQGNEDCTENTDNLPGCKIQRKVRLLDGO-QANNEPSELDK 594
QY 594 AEPD-KRTEPTTQEBNRICSSPVOSLLDLFQTSSEKSEFLGFTSTYKSGICNVLDIWE 652
DB 594 AEPD-KRTEPTTQEBNRICSSPVOSLLDLFQTSSEKSEFLGFTSTYKSGICNVLDIWE 652
QY 653 ENSDNLTAFFSSPSTSTGTG 674
DB 653 ENSDNLTAFFSSPSTSTGTG 674
QY 655 ENSSSLSTFFSSPSASTGTG 676
DB 655 ENSSSLSTFFSSPSASTGTG 676

```

RESULT 5

090241 PRELIMINARY; PRT; 321 AA.  
 AC 090241;  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE 14 DAYS EMBRYO LIVER CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,  
 CLONE:4432409B02, FULL INSERT SEQUENCE.

Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN  
 RP  
 SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC LIVER;  
 RC MEDLINE=21085660; PubMed=11217851;  
 RA Kawai T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Akawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Atzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,  
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schmitt L.M., Strubill P., Suzuki R., Tomita M., Wagner L., Mashio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,  
 RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontutski S.,  
 RA Hayashizaki Y.,  
 RA Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 RL EMBL: AK014480; BAB29383.1;  
 SQ SEQUENCE 321 AA: 36324 MW: 7418172CF52A4579 CRC64;

Query Match 37.18; Score 1303.5; DB 11; Length 321;  
 Best Local Similarity 80.5%; Pred. No. 4.4e-76;  
 Matches 248; Conservative 23; Mismatches 36; Indels 1; Gaps 1;

QY 1 MNSGAMRHSKGFQGGIOVKNRNPRLSLKLTDRNRPKSKCKPLMGKVFYLDLPSTVI 60  
 DB 1 MNELETHIRHSKAPLPGGIODRNEKNRPSLSKLADNRLKSKYKRLGKIFVLDLPSTTI 60  
 QY 61 SEKLDKIDLDGVRVEEFLSKDISYLSNKKKFAQTLGRISVPSPESAVTAETTSPI 120  
 DB 61 CEKLDKIDELGRVEEFLSKDISYFVSNKKFAQTLGRISVPSPESAVTAETTSPI 120  
 QY 121 PSHDGSFSPDVCYLSRGLKLEKAIKDHFIPNSILSNALSMGVKILHIDIRYIE 180  
 DB 121 PSHDGSFSPDVCYLSRGLKLEKAIKDHFIPNSILSNALSMGVKILHIDIRYIE 180  
 QY 181 OKKRELYLLKSSYVRDGGKRVGSAQKTRTGRLKPFVYEDMSQLYRPYLDLPST 240  
 DB 181 OKKRELYLLKSSYVRDGGKRVGSAQKTRTGRLKPFVYEDMSQLYRPYLDLPST 240  
 QY 241 FINSYDOKPSPDVCYLSRGLKLEKAIKDHFIPNSILSNALSMGVKILHIDIRYIE 300  
 DB 241 CINFYDOKPSPDVCYLSRGLKLEKAIKDHFIPNSILSNALSMGVKILHIDIRYIE 300  
 QY 301 OKTDELET 308  
 DB 301 OKTDELET 307  
 RESULT 6  
 QY2M6 PRELIMINARY: PRT; 234 AA.  
 AC QY2M6;  
 DT 01-NOV-1999 (TREMblrel. 12, Created)  
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE ACTIVATOR OF S PHASE KINASE.  
 GN ASK/ H37  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI\_TaxID=9606;  
 RN  
 RP  
 SEQUENCE FROM N.A.  
 RA Kumagai H., Sato N., Yamada M., Mahony D., Seghezzi W., Lees E.,  
 RA Araki K., Masai H.,  
 RA "A Novel Growth- and Cell Cycle-Regulated Protein, ASK, Activates  
 Human Cdc7-Related Kinase and is Essential for G1/S Transition in  
 RT Mammalian Cells."  
 RL Mol. Cell. Biol. 0:0-0(1999).  
 DR EMBL: AB028070; BAB78327.1;  
 DR InterPro: IPR001357; BRCT.  
 DR SMART: SM00292; BRCT; 1.  
 SQ SEQUENCE 234 AA: 26124 MW: 50357B9CF8472BC CRC64;

Query Match 33.3%; Score 1170; DB 4; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-67;  
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSGAMRHSKGFQGGIOVKNRNPRLSLKLTDRNRPKSKCKPLMGKVFYLDLPSTVI 60  
 DB 1 MNSGAMRHSKGFQGGIOVKNRNPRLSLKLTDRNRPKSKCKPLMGKVFYLDLPSTVI 60  
 QY 61 SEKLDKIDLDGVRVEEFLSKDISYLSNKKKFAQTLGRISVPSPESAVTAETTSPI 120  
 DB 61 SEKLDKIDLDGVRVEEFLSKDISYLSNKKKFAQTLGRISVPSPESAVTAETTSPI 120  
 QY 121 PSHDGSFSPDVCYLSRGLKLEKAIKDHFIPNSILSNALSMGVKILHIDIRYIE 180  
 DB 121 PSHDGSFSPDVCYLSRGLKLEKAIKDHFIPNSILSNALSMGVKILHIDIRYIE 180  
 QY 181 OKKRELYLLKSSYVRDGGKRVGSAQKTRTGRLKPFVYEDMSQ 227  
 DB 181 OKKRELYLLKSSYVRDGGKRVGSAQKTRTGRLKPFVYEDMSQ 227

RESULT 7  
 QY9R5 PRELIMINARY: PRT; 1695 AA.  
 AC QY9R5;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE CHIFON.  
 GN CHIF OR CHIFON OR BG:DS09218.2 OR CG5813.  
 OS Drosophila melanogaster (fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN  
 RP  
 SEQUENCE FROM N.A.  
 RC STRAIN=CANTON-S;  
 RA Landis G.N., Tower J.;  
 RA "The Drosophila chifon gene is required for chorion gene  
 RT amplification and is related to the yeast Dbf4 regulator of DNA  
 RT replication and cell cycle."  
 RL Development 126:0-0(1999).  
 DR EMBL: AF158178; AAD48779.1;  
 DR FlyBase: FB0000307; chif.  
 DR InterPro: IPR000637; AT-hook.  
 DR Pfam: PF00178; AT-hook; 1.  
 DR SMART: SM00384; AT-hook; 1.  
 SQ SEQUENCE 1695 AA: 18080 MW: 1409DD8A1587C4B0 CRC64;

Query Match 7.88; Score 273; DB 5; Length 1695;  
 Best Local Similarity 21.8%; Pred. No. 3.8e-09;  
 Matches 154; Conservative 100; Mismatches 212; Indels 242; Gaps 32;

QY 27 PSLSKLTDRNRPKSKCKPLMGKVFYLDLPSTYISKLDKIDLDGVRVEEFLSKDISYL 86  
 DB 32 PKYVIRSK-----RPLCHFKFYLDICDQHLAKRISDIKALGHLGHLFSLDDITFR 83

```

QY 87 ISNKEAKFAQTIGRISVPSPESAYTAETTSPPHSDGSSFK-----SPDYVCLSRCKL 141
DB 84 VTDPE-----VIGTSGTPTPTST-PETPTSHQONDGSRKRNOROSRADALISRRR 137
QY 142 LVERAKIDHIPSNSILSNALSMGVKLHIDIRYYIEQKKEI--YLKRSSTVRDG 199
DB 138 STGVVNSGNSPTTSLKRSYTIW-----CTDVAORFIKRLQTELMKYL-----E 182
QY 200 GKRKSGAKKRTG---RLKRPYKVEDMSOLYRPF---LQLTNMPINYSIQPCSPF 253
DB 183 GKRGGGGSGTASPHHDLKQYKIESVKRNPYPYHLIKQPDWPKIDLSSED--GAF 240
QY 254 DV-----DKPSSMOKOTGYKLRIDGDKYGGGSIQLO-----LKEKKK----- 293
DB 241 RLILKSTKDKESHSTKTRPLGSRTSQKD-KOAGEBAPLQHPSLQELKQSAIIPSPRSN 299
QY 294 -----GYCECLQKVEDLETHLSEQRNFAOS-----NOY 324
DB 300 CREPIDSEKGGGVCCEICKLEYDILNIHLSQKHILFAKNNDNLALDTLLQSSADVNR 359
QY 325 QVVDIYKLVDFVE-----YEKOTP---KKRI--KYSVGLSPVASV-- 365
DB 360 LEEBPVSELDMDVDESLSNEELQSPRQRPSPALREKSKRITKGHSEKFGVAVASPO 419
QY 366 -----LKTTEKEVVELQHSQKDCQEDDTV-----KEQN----- 396
DB 420 TPEPKAKVQNSPQSGISELQ---QEHPTAAAPTPTNSGRRTQNGSLSPKRAMLP 476
QY 397 -FLYKTOETEKRLTISEP-----IPHS-----NELRGINEMKSNKS 435
DB 477 SSITKYVETRE---CATPPRGKGRPNNOVDSLIYKPKIKOTELQKRLNGE----- 526
QY 436 MLSTAEDDIRQNF---TQLPLKKNQECILDISEHTLSENDLELRVDHYKNQIASVH 491
DB 527 -----AENFMEPRAPVPTRSSSELPTVDVROQTSD-----VKGYS 563
QY 492 VSDSTDSNGSQPKQKSTVYV-----FPADLKAKKDLHSFTHDG 532
DB 564 ISSASLPTSTSEALTKESSGLPTSTIRKRAQAVGRRKRVKGAAGVDFPQROI-----STG 617
QY 533 LITNSSEHTLQAKAPFHTPEEPNECDPKMNDSLPSCGIHKKVKI 580
DB 618 SSSSNSMQQR-----FPSAPLQPEE-----GPQDPKPOLKIKI 651

```

```

RESULT 8
Q9NKS3 PRELIMINARY; PRT; 1695 AA.
AC Q9NKS3;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CHIF PROTEIN.
GN CHIF OR BG:DS09218.2 OR CG5813.
OS Drosophila melanogaster (fruit fly)
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydriidae; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Y AND CN BW SP.
RA MEDLINE=99403001; PubMed=10471707;
RA Ashburner M., Miska S., Roote J., Lewis S.E., Blazey R., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA Palazolo M., Reese M.C., Spradling A., Tsang G., Wan K., Whitelaw K.,
RA Celniker S., Rubin G.M.;
RT "An exploration of the sequence of a 2.9-Mb region of the genome of
RL Drosophila melanogaster: the Adh region.";
RN Genetics 153:179-219(1999).
[2]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN-Y AND CN BW SP.
RA Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazey R.G.,
RA Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
RA Faifan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA Houston K.A., Humastli S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomoton M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon S., Paley J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sechi H., Snir E., Svirkas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zieran L.U., Rubin G.M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolintsov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos P., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dubin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostali D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jastil M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paley J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Sidenklamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,
RA Zheng X.H., Zhong F.-N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003416; AAF45011.1; -
DR EMBL: AE003416; AAC22437.1; -
DR FlyBase; FBgn0000307; chif.
DR InterPro; IPR000637; AT_hook.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02178; AT_hook_1.
DR SMART; SM00384; AT_hook_1.
DR PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN.1.
SO SEQUENCE 1695 AA; 188046 MW; B3858353C3DAFA0 CRC64;

```

```

Query Match 7.8%; Score 273; DB 5; Length 1695;
Best Local Similarity 21.8%; Pred. No. 3.8e-09;
Matches 154; Conservative 100; Mismatches 212; Indels 242; Gaps 32;
QY 27 PSLKLTQDNRPESKCKPLMGKVFYLDPSVTYISEKIQKIDKIGVGEFLSKDISYL 86
DB 32 PKVYIKSK-----RPLCHFKEFYLDICDQHLAKRTESDKALGHIHFEFLSDITHF 83
QY 87 ISNKEAKFAQTIGRISVPSPESAYTAETTSPPHSDGSSFK-----SPDYVCLSRCKL 141

```

```

Db 84 VTDKPE-----VIGGTSRGPPT-PCPTSHYQDGSARKPNQGRADALISRYR 137
142 LVEKAIKDHDFIPNSILSNALMSGVKLIHIDIRYIEBKKEL---YLLKSSSYVMDG 199
138 STGVVNSGSIPTTSIKSYIY-----QTDVAGRIKRIQTELKQYL-----E 182
200 GKRVSQAOKTRTG---RLKPFVAVEDMSOLYRPF---LQITNPFINSIQRCPSPF 253
183 GKRGGGGSGTSASPHIITQIKOYVIESVKNNRYHLIKOPDDPKIDLSSE--GAF 240
254 DV-----DKPSSMOKQTVKRLIQTDGDKYGGTSTQIQ--LKEKKK----- 293
241 RLTKRSKTKDKESHSMTRKPLGSRISQKD--KQAGEAKPLOHPSLOELKQSAIPNSPSN 299
294 -----GYCCCLQKYDELETHLSEOHNFPAOS-----NOY 324
300 CREPIDSEKOGGVCEICLKVEDIINILQSKDHLELAKSDNFALDTLIQSDAVNRF 359
325 QVVDIVSKIVPFVE-----YEKDRP---KKKRI---KYSVGLSPVASV-- 365
360 LEEPPVSELDMDVDESLNEELQSPRQSPALREKSKRTIGKSSSEKQGVAVASPO 419
366 -----LKTROKKEVLEIHSOKDQOEEDTV-----KEON----- 396
420 TPPGAKKVGNSPGSLSELQ---QEHPTTAATPTTNSGRKRTQNSGLSPPKRAMLP 476
397 -FLKKEOTETKLLFISF-----IPHS-----NELGLNEKMSKCS 435
477 SSITKVETREE---CATPPRGGRPNQVDSPLVYKOTKROTELQRLNGE----- 526
436 MLSTAEEDIRQNF---TQPLHKKKQCIIDISEHLSLNDLELKVNDHYKCNQASVH 491
527 -----AENMFPPETAAPTTRSSSELPDVPDQRTSD-----VGRYS 563
492 VSDPSTNDSGQKOKSDTVL-----FPAKDKERDLSTFTHDSG 532
564 ISSASLDTSTSEATEKSSGLPTSIKRAQAVGRRKRVGAQAQDVFQRL-----STG 617
533 LITNSSQEHITVQAKAPFPTPEEPNECDPKMNDSPISKRHKVY 580
618 SSSNSMQR-----FPSAPIQPEE-----GPOFQPKPOLKIKI 651

```

```

RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunker B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodak A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Howell T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howard T.J., Mei M.-H., Ibbagyan C.,
RA Jødal M., Kalish F., Karpen G.H., Ke Z., Kennison J.D., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Klup J., Lin Z.,
RA Liao X., Lei Y., Levitsky A.A., Li J., Li Z., Ling X., Lin X.,
RA Luo X., Matei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Millaushina N.V., Mobarry C., Morris J., Moshell A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M.,
RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen T.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spredling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtikas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhou S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AEO03650; AAF53530.1;
DR FlyBase: FBgn0000307; ch1f.
DR InterPro: IPR000637; AT_hook.
DR Pfam: PF02178; AT_hook.1
DR SMART: SM00384; AT_hook.1
SQ SEQUENCE 1711 AA; 189216 MW; 4CF179D974817BDA CRC64;

```

Query Match 7.8%, Score 273; DB 5; Length 1711;  
 Best Local Similarity 21.8%, Pred. No. 3, 8e-09;  
 Matches 154; Conservative 100; Mismatches 212; Indels 242; Gaps 32;

```

OY 27 PSLKSLKTDNRPEKSKCPKMGKVFYLDLPVYISEKLDKIDLGRAVEELKDISYL 86
Db 32 PKYAVIKSK-----RLCLHFKEFYLDICDHOAKRIESDIALGCHLEFFLSDDITF 83
84 VTDKPE-----VIGGTSRGPPT-PCPTSHYQDGSARKPNQGRADALISRYR 137
142 LVEKAIKDHDFIPNSILSNALMSGVKLIHIDIRYIEBKKEL---YLLKSSSYVMDG 199
138 STGVVNSGSIPTTSIKSYIY-----QTDVAGRIKRIQTELKQYL-----E 182
200 GKRVSQAOKTRTG---RLKPFVAVEDMSOLYRPF---LQITNPFINSIQRCPSPF 253
183 GKRGGGGSGTSASPHIITQIKOYVIESVKNNRYHLIKOPDDPKIDLSSE--GAF 240
254 DV-----DKPSSMOKQTVKRLIQTDGDKYGGTSTQIQ--LKEKKK----- 293
241 RLTKRSKTKDKESHSMTRKPLGSRISQKD--KQAGEAKPLOHPSLOELKQSAIPNSPSN 299
294 -----GYCCCLQKYDELETHLSEOHNFPAOS-----NOY 324
300 CREPIDSEKOGGVCEICLKVEDIINILQSKDHLELAKSDNFALDTLIQSDAVNRF 359
325 QVVDIVSKIVPFVE-----YEKDRP---KKKRI---KYSVGLSPVASV-- 365
360 LEEPPVSELDMDVDESLNEELQSPRQSPALREKSKRTIGKSSSEKQGVAVASPO 419
366 -----LKTROKKEVLEIHSOKDQOEEDTV-----KEON----- 396
420 TPPGAKKVGNSPGSLSELQ---QEHPTTAATPTTNSGRKRTQNSGLSPPKRAMLP 476
397 -FLKKEOTETKLLFISF-----IPHS-----NELGLNEKMSKCS 435

```

```

Db 477 SSIVKVTREE-----CATPPRGRRPNQVDSPLIVKFOKIRQELQRLNGE----- 526
QY 436 M1STAEEDIRONF-----TOLPLHKKQECILDISERTISENDLELRVDHYCNIOASVH 491
Db 527 -----AENFMPPRTAVPTTRSSSELPTVDROTSD-----VGRYS 563
QY 492 VSDFTDNGSGOPKOKSDVLT-----FPAKDLKEDLSIFTHDSG 532
Db 564 ISSASLDTSTSEAEKESGLPTSIKRAQAVGRRKRVGGAAADYFOROL-----STG 617
QY 533 LTTINSSOEHLTVOAKAPHTPPEEPNECDFKNMDSLPSGKIHRKYKI 580
Db 618 SSSSNSNOOR-----FPSAPIQPEE-----GPOPPKPOLKIKI 651

RESULT 10
QY09R4 PRELIMINARY; PRT; 1711 AA.
AC 0909R4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CHIEFON-2.
GN CHIEF OR CHIEFON OR BG:DS09218.2 OR CG5813.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON-S;
RA Landis G.N., Tower J.;
RT "The Drosophila chifton gene is required for chorion gene
RT amplification and is related to the yeast Dbf4 regulator of DNA
RT replication and cell cycle.";
RL Development 126:0-0(1999).
DR EMBL; AF158179; A048780.1; -.
DR FlyBase; FBgn000307; chif.
DR InterPro; IPR000637; AT_hook.
DR Pfam; PF02178; AT_hook; 1.
DR SMART; SM00384; AT_hook; 1.
SQ SEQUENCE 1711 AA; 189250 MW; B7D0F95517C4B9A9 CRC64;

Query Match 7.8%; Score 273; DB 5; Length 1711;
Best Local Similarity 21.8%; Pred. No. 3.8e-09;
Matches 154; Conservative 100; Mismatches 212; Indels 242; Gaps 32;

QY 27 PELKSLKTDNRPEKSKCKPLMGKVFIYLDPSVTISEKLOKIDKLGGRVEFLSDISYL 86
Db 32 PRVKVTKSK-----RFLCHFKEFYLDICDHLAKRIESDIKALGHEFFLSDDITHP 83
QY 87 ISNKEAKFAQTLGRISPPSPESAAYTAETTSPPHSHDGSSEK-----SPDVYCLSRGL 141
Db 84 YTDKRE-----VIGGTSQPTPTPT-PTGPTSHYQOONSARKPNQROGRAALISRYAR 137
QY 142 LVEKAIKDHDFIPNSIISNALSMGVKILIHDDIRYIEQKKEL--YLLKSSSTVRDG 199
Db 138 STVGAVNNGNSTPTTSLKSYTIW-----QTDYAOFEIKRIQTELKOYL-----E 182
QY 200 GRRVSGAQKTTTG---RLAKRPVVEEDMSQLXRPY---LDLTNPFYINYSIOKFCSP 253
Db 183 GKREGGGSTASPHHIDIKOYVKIESYKRVYRPHYHLIKOPDMPKIDLSSE--GAF 240
QY 254 DV-----DKPSSMOKOTQVRLIOTDGDYGTSTIOQ---LKEKKKK----- 293
Db 241 RLUTSKTKKDKKHSMTKRPKDSRTSQKD--KQAAEGEAKPRLQHSISLOELKQSAIPNSPRN 299
QY 294 -----GYECCLQKYTEDETHLLSQHNRNPAQS-----NQY 324
Db 300 CREPIDSEKGGVCEICLEFYDILNIHLSQKHDELFAKNSDNFLADLTLOSADVNR 359

```

```

QY 325 QYVVDIVSKLVDFVE-----YEKDTP---KKRI---KYSVGSLSPVASV--- 365
Db 360 LEEPESELDVDVDVDSLNEELQSPRRQSPALREKSKRITKGSSEKFOGVAVASPO 419
QY 366 -----LKTEQKEKVEYLQHISOKDCOEDDTV-----KEON----- 396
Db 420 TTFPPAKKVKQNSPGLSELQ---QEHPTTAAATPTTNSGRRKTONSLSPPKRAMLP 476
QY 397 -FLYKETOETEKLLAFISPP-----IPHP-----NELRLGNEKMSNKS 435
Db 477 SSIVKVTREE-----CATPPRGRRPNQVDSPLIVKFOKIRQELQRLNGE----- 526
QY 436 M1STAEEDIRONF-----TOLPLHKKQECILDISERTISENDLELRVDHYCNIOASVH 491
Db 527 -----AENFMPPRTAVPTTRSSSELPTVDROTSD-----VGRYS 563
QY 492 VSDFTDNGSGOPKOKSDVLT-----FPAKDLKEDLSIFTHDSG 532
Db 564 ISSASLDTSTSEAEKESGLPTSIKRAQAVGRRKRVGGAAADYFOROL-----STG 617
QY 533 LTTINSSOEHLTVOAKAPHTPPEEPNECDFKNMDSLPSGKIHRKYKI 580
Db 618 SSSSNSNOOR-----FPSAPIQPEE-----GPOPPKPOLKIKI 651

RESULT 11
QY0912 PRELIMINARY; PRT; 170 AA.
AC 090912;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CDNA FLJ13087 F15, CLONE NT2RP302099.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Magatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takehashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y.,
RA Ninomiya K., Iwayanagi T.;
RA "NEO human cDNA sequencing project.";
RT Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AK023149; BAB14431.1; -.
SQ SEQUENCE 170 AA; 18392 MW; C93DEF02A59B282E CRC64;

Query Match 5.9%; Score 208; DB 4; Length 170;
Best Local Similarity 36.4%; Pred. No. 3.2e-06;
Matches 55; Conservative 22; Mismatches 44; Indels 30; Gaps 4;

QY 21 KNEKNRPSLSLKTDRNRPKSKCKPLMGKVFIYLDPSVTISEKLOKIDKLGGRVEEFLS 80
Db 35 KCKNSPFGARK-----HPPSGKSFYLDLPAGNLFILTAIOQLGGVIGFLS 82
QY 81 KDISYLSNKKKKAFAQTLGRIT-----SPVSPESAAYTAETTSPPHSHDGSSEKSPDYTC 135
Db 83 KEYSYVSSRRREK-AESSGKSHRGCPSPSPSEVRVETASAMVDKPSHPSPKPDVSV 141
QY 136 LSRGLLVEKAIKDHDFIPNSIISNALSMG 166
Db 142 LSRGKELLQKALR-----NQVSMG 160

RESULT 12
QY07380 PRELIMINARY; PRT; 1790 AA.
AC 007380;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CHIEFON-2.
GN CHIEF OR CHIEFON OR BG:DS09218.2 OR CG5813.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON-S;
RA Landis G.N., Tower J.;
RT "The Drosophila chifton gene is required for chorion gene
RT amplification and is related to the yeast Dbf4 regulator of DNA
RT replication and cell cycle.";
RL Development 126:0-0(1999).
DR EMBL; AF158179; A048780.1; -.
DR FlyBase; FBgn000307; chif.
DR InterPro; IPR000637; AT_hook.
DR Pfam; PF02178; AT_hook; 1.
DR SMART; SM00384; AT_hook; 1.
SQ SEQUENCE 1711 AA; 189250 MW; B7D0F95517C4B9A9 CRC64;

```



DT 01-NOV-1996 (Tribblel. 01, Created)  
 DT 01-NOV-1996 (Tribblel. 01, Last sequence update)  
 DT 01-JUN-2001 (Tribblel. 17, Last annotation update)  
 DE HYPOHETICAL 206.5 KDA PROTEIN IDL058W.  
 GN USOI OR IDL058W.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 NCBI\_TaxID=4932;  
 RX NCBI\_TaxID=4932;  
 RP SEQUENCE FROM N.A.  
 RA Blocker H., Brandt P.;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; 274105; CA98621.1; -;  
 DR EMBL; 274105; CA98620.1; -;  
 DR SGD; 50002216; USOI.  
 DR InterPro; IPR002017; Spectrin.  
 SQ SEQUENCE 1790 AA; 206450 MW; 9006254455A52EE CRC64;

Query Match 5.3%; Score 187; DB 3; Length 1790;  
 Best Local Similarity 19.9%; Pred. No. 0.0013;  
 Matches 150; Conservative 133; Mismatches 273; Indels 198; Gaps 31;

QY 2 NSGAMRIHSKHFGGIGVKNKRPISLKTDRPEKSKCKPLMKGVFYLDLPSTVTS 61  
 DB 978 NSSLKAVEESKNSSTSLNKNIDMSQEN-----PQIERGSIEN 1023  
 QY 62 -EKIQDKIDGCHVEFLSK-----DISVLISNKKAKFA--QTIGRI SPVSP 108  
 DB 1024 ISQLKTTISDLEQTEKRIKSDSSKDEYESQISLKKLETATANDENVNKISLTYT 1083  
 QY 109 ESAVYAEFTTSPHSDSSKSPDVCLSRGLVKAIRKDHDFIPNSISLNAISMGV 168  
 DB 1084 REELAEELAA-----YKLNKLETKLETLS-----EKALKE--VKENE----- 1119  
 QY 169 IIAIDIRYIEOK---KKELYLLKSSSTSVRDGKRVGSAOCTRTGRKLPYKVED 224  
 DB 1120 -EHLKEEIQLEKATETKQOLNSLANLESLEKEHDLAQLKKYEEQIANEROYNEE 1178  
 QY 225 MSQLYRPYIQLJNMPFINSIQKPCSPFDV--KPSMOKOTQVRLIQTQDQRYGCT 281  
 DB 1179 ISQLND---ETSTQENESIKRKNDELEGEVAKMAKSTSEOSNLK-KSEID----- 1226  
 QY 282 STIQQLKERRKGGYC-----ECCLOKYE--DIEETHLSSEQH 315  
 DB 1227 AALDQIKELKKNETNASLESIKSVESEYVRIKELQDECNFEKEVESELEKLASED 1286  
 QY 316 RNF-----AOSNOYOVVDIVSKLVDFVEYEKDTPKKRIKRYVGSLSPVASVYLKTEQ 371  
 DB 1287 KNSKYLELOKSESEKIKELDAKTTELKIQLEKRTNLSAKKESSELSR-----LKTSS 1341  
 QY 372 KKKVELQHSOKDCQEDDTYKQNFYKETOETEKLL-----FISEPIPHSNELRGL 426  
 DB 1342 EER-----KNNEEQLKKNEDIQKNOAFERKIKLNCSSSTIQOYSEKINTLEDE 1393  
 QY 427 NERKSNKCSMLSTAEDDIRONFTQPLH-----KNKOCILIDISEHPLS----- 470  
 DB 1394 LRILOENELAKETIDYRSELEKVSLSNDELLEEKONTISLODEILSKDKITRNDEK 1453  
 QY 471 -----ENDLEELR-----VDHYKCNQI-----ASY 490  
 DB 1454 LLSIERONKRRLSELKQLRAQESKAKVEEGIKLLEBSSKEKAELEKSKEMMKLEST 1513  
 QY 491 HVSDFSTNDSGQPKQSDTVLPANLKEKDLHSIFTHDSGLIT-INSSQE-----H 542  
 DB 1514 IESNTELEKSSMETIRTSDEKLSQSKSAEEDIKMLQHEKSDLSIRINESKDIIEELK 1573  
 QY 543 LTVQAK--APFHTPEEPNECDKKNMDSLPSGKIRKRYKIIIGGNRKNLEPNAAFDKRT 600  
 DB 1574 LRIEAKSSGELELEYQELNNAQEKI-----RINAENTVL--KSKLEDIERELK--DKQA 1624  
 QY 601 EF-IYQENRICSSPVOST--LDLFQITSEKSE 630

DB 1625 EIKSNOEKEKELTSRLKEFQELDSITQAKAKSE 1658  
 RESULT 13  
 ID 09AHK6 PRELIMINARY; PRF: 1173 AA.  
 AC 09AHK6;  
 DT 01-JUN-2001 (Tribblel. 17, Created)  
 DT 01-JUN-2001 (Tribblel. 17, Last sequence update)  
 DT 01-JUN-2001 (Tribblel. 17, Last annotation update)  
 DE LMP1.  
 GN Borrelia burgdorferi (Lyme disease spirochete).  
 OS Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.  
 OC NCBI\_TaxID=139;  
 RX NCBI\_TaxID=139;  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-HB19;  
 RA Dunn J.J.;  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF305609; AAK1801.1; -;  
 DR SEQUENCE 1173 AA; 134287 MW; F0713ADF2E2311DC CRC64;

Query Match 5.2%; Score 182; DB 2; Length 1173;  
 Best Local Similarity 19.4%; Pred. No. 0.0016;  
 Matches 160; Conservative 144; Mismatches 290; Indels 232; Gaps 43;

QY 22 NEKNRPSLSLKTDRNPKSKCP--LMGVF--YLDLPSTVISEKIQDKIDG----- 72  
 DB 249 NNNNTTSLKTPSKQSESELSPPSTIIGKITRY-----SYLKRLYEIILDDITGRV 304  
 QY 73 -----GRVEEFLSKDIS-----YLISNKKAKFAQ-----TLGRISPPSPFE 109  
 DB 305 TLGNRLKLELIKGLSKRFOYNELNSKNKESNLLILKIDIDEPILNIPKDPYK 364  
 QY 110 SAYVYAEFTTSPHSDG---SFKSPDVCLSRGLVKAIRKDHDFI--PNSISLSNA 162  
 DB 365 ETEFDQDKRRPQHPGDLKSKVHSIKPIDENTKSR--QOAIKIDNLEFLKNNPNDQASKT 423  
 QY 163 LSWGVKILHIDIRYIEQ--KKELYLLKSSSTSVRDG--KRVGSAOCTRTGRKLP 218  
 DB 424 LAQANKIQHLEDLSRVHSIKPIDENTKSRQOAIKIDNLEFLKNNPNDQASKTTLAQAANK 483  
 QY 219 FVKVEDM--SQLY--RPYIQLIN---MPTINSIQKPCSPFDVDPKPSMOKOTQVRL 270  
 DB 484 IQHLEDLSKSVYSIRPIDENTKSRQOAIKIDNLEFLKN--NPNDQASKTTLAQAANKIHL 541  
 QY 271 IOTDQDYGSTSIQLQLEKRRKGYCECLOKYEDELTHLL-----SEQRNFAOSNOYO 325  
 DB 542 EDLKSVMHSIRPIDENTKSRQOAIKIDNLEFLKN--NPNDQASKTTLAQAANKIOT 593  
 QY 326 VVDIVSKL-----VFDEVEYEKDTPKKR-----IK 352  
 DB 594 HLEDLSKSVYSIRPIDENTKSRQOAIKIDNLEFLKNNPNDQASKTTLAQAANKIQHLEDL 653  
 QY 353 YSVGSLFSVASVYLKTEQ--KEVELQHSOKDCQEDDTYKQNFYKETOETEKLL 410  
 DB 654 SKVYSIRPIDENTKSRQOAIKIDNLEFLKNNPNDQASKTTLAQAANKIQHLE--DLKSVH 711  
 QY 411 FISEPIPHSPNE-----LQGLNEMSN-----KCSMLSTAEDDIRONFTQPL 453  
 DB 712 ST-RIPIENTKSRQOAIKIDNLEFLKNNPNDQASKTTLAQAANKIQHLEDLSKSVYSIR 770  
 QY 454 H-----KNKOCILIDISE-----HTL-----SENDELLE-----RV 479  
 DB 771 DLENTKSRQOAIKIDNLEFLKNNPNDQASKTTLAQAAYENNGLDAENAYETIKITLNTQE 830  
 QY 480 DHYKCN-----QASVHVSDFSTNDSGQPKQSDTVLPANLKEKDLHSIFTHDS 531  
 DB 831 DHYKGIIRFLKLYKHEHSISFD-----QTIKIDPKHKRALHAK 869



```

OY 532 G--LITINSSOEHL-----TVOAKAFPHTP-----PEEPNE-----CDFK---NMDSL 569
DB 870 GIALMLMKKKKAISFEKAIQIDKNITAYQKIAEKKMGDMQOAAFRKNNAYNLCKN 929
OY 570 PSQIHRKVKII--LGRNRENLEP---NAEPDKRTEF-----ITQENRRCSSPVO 616
DB 930 PNVAL--KAGIYSNNLG--NFKOSEEYLNFFNANNAKKPMEIATYNLSIAKPFENNKLEESLE 986
OY 617 SLDDIFQTSSEKSEPLGFTS--YTEKSGICVLDIWE---BENDSN 657
DB 987 TINKRAIDNPEKSEYLYLKASINLKKENYONAIISLYSLVTEKNPEN 1032

RESULT 14
OY 09AV25 PRELIMINARY; PRT: 1578 AA.
AC 09AV25;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE PUTATIVE KINESIN-RELATED PROTEIN.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_Taxid=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, NIPPONBARE;
RA Buehl C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Burr P.C.,
RA Hsiao J., Zisman V., Pal G., Bowman C.L., Fujii C.Y., Vanken S.E.,
RA Bowman C.L., Craven B., Utechtack T.R., Khalak H., Feldblum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RT *Oryza sativa chromosome 10 BAC OSJNBa000104 genomic sequence.*;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC025783; AAR20041.1; -
SQ SEQUENCE 1578 AA: 178947 MW: CBB7ELDB68A821A0 CRC64;

Query Match 5.2%; Score 181.5; DB 10; Length 1578;
Best Local Similarity 19.9%; Pred. No. 0.0025;
Matches 152; Conservative 109; Mismatches 256; Indels 245; Gaps 38;

OY 19 QVKNKKNPRLSKLK---TDNRPEKSKCKPLMGKVFYLDLPSVTISER--LQDKDKDGG 73
DB 340 QKRTKRLKQGETLTKKRECADSKQSELE-----LEL-SISISESDSLKQTEIEELKR 390
OY 74 RVEEFLSDIDYILISNKKKFAQTLGRISPVSPESAVTAETTSRPHSHDSSFKSPDT 133
DB 391 SLEEVYTA-----QTISSR-----SPRSGDATELQK--EVEDDVQFLKESN 428
OY 134 VCLG-----RGLLVEKA-----IKDHDFIPSNLSILNAL 163
DB 429 ASLATOLKKAQENAIETYSIIQELBETIEVQRAELISNLSHTSDLDHEVSPNLLIQEDV 488
OY 164 SWGKVI-LHIDIRIYIQKKKELYLLKKSSIVDGGKRVGSGQKRTGRLKLPKPVAV 222
DB 489 EMARVVSJKEDELLMLRKRIKIDMLHV-----ENPNGRSSGA----- 524
OY 223 EDMGSLVPFYQL-TNMPFINYSIO---KPCSPFDVCKPSSMOKOTQV----- 267
DB 525 -----TYLELEKEDFLVKIQLQELKDCSELTDLELITYLKEKSEVAKEDPSV 575
OY 268 --KLRTQDGDYKYGTSIQLQLEKKKKGYCECCLOKYEDLETHLL-----SEQRNFAQ 320
DB 576 PNSEVSESGD-----LSDRLTSKVK--YLE--TKCADLELKLISPSSESELEPKKQ 624
OY 321 SNQYVVD--DIVKLV-----VFDVVEYKQTPPKKRIKYSVGSLSPVASVYLKTE 370
DB 625 KSOELKRLRIETELSLDRKLKSGFHALMEEGDTPSAKSKLKSE-----KIDE 672
OY 371 QKEKVELHISQKQDQEDDTYKQONFLYKETOETEKTL-LFISDFIPHSNELLGLINEX 429

```

```

DB 673 NDNKTEL-----DALRSTVLLKBEEL--ESLQSKKMEPSISE--IMNEKNKLEELLE 723
OY 430 MSNCKSMJSTAEDDRQNFQTLPLKKNQCECLIDISEHTLSENDEELRVHYKCNIOAS 489
DB 724 SLKECSITACIDEMREBELLL-----TSSIDSHVSTNNVLETITELESQVMLE 774
OY 490 VHYSDSFQDN-----SGSQPKQSDTVLPFAKDLKEDLHSITTHSGITINSSQEH 542
DB 775 LHSIKLEHNEVLESEFTIGLSOL--TYL-----ANKELSMQMDERSRLTNKDEL 826
OY 543 LTVQA-KAPFHTPEEPNE--CDFKN-MDSLPSGKIHRRKVIILGR---NRKNMJE--- 591
DB 827 EGVENQKVELKQMDERSLITNLKDELEQYEAQKVELKQMDERSRLITNLKDELEVE 886
OY 592 -----PNAEPDKRTEFTQENRRCSSPVOSLDLF 622
DB 887 AQVELKENQLESHRRRLSEVOEDSEALRRSNAKLOATVDHVAEE---CKSIQTLTADL- 941
OY 623 QTSSEKSEFLGFTSYTEKS-----GICNVLDIMEENS 655
DB 942 --KKQLEVHGVAHLEQLEQSKRKRTMDPCKTLESLAKUS 981

RESULT 15
OY 049545 PRELIMINARY; PRT: 1344 AA.
AC 049545;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMblrel. 08, Last annotation update)
DE Lmp1 AND Lmp2 GENES.
OS Mycoplasma hominis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmales; Mycoplasma.
OX NCBI_Taxid=2098;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PG21;
RX MEDLINE=95104998; PubMed=7806360;
RA Ladefoged S.A., Birkelund S., Hauge S., Brock B., Jensen L.T.,
RA Christiansen G.;
RT *A 135-kilodalton surface antigen of Mycoplasma hominis PG21 contains
RT multiple directly repeated sequences.*;
RL Infect. Immun. 63:212-223(1995).
DR EMBL: X81475; CA57228.1; -
SQ SEQUENCE 1344 AA: 149404 MW: 6E0105F7365AF8CF CRC64;

Query Match 5.0%; Score 177; DB 2; Length 1344;
Best Local Similarity 19.1%; Pred. No. 0.004;
Matches 132; Conservative 132; Mismatches 256; Indels 170; Gaps 30;

OY 19 QVKN-----EKNRPSLSIKTDNRPKSKCKPLMGKVFYLDLPSVTISEKLO----- 65
DB 221 EIKNMQAVASNNITASQMSAKSS-----LDAKVAETTKLETTNNKQKE 273
OY 66 --KDKLQGRVEEFLSDIDYILISNKKKFAQTLGRISPVSPESAVTAETTSRPHS 122
DB 274 AKFNELKQTRNQIQEFIN-----TNKNNPYSSELISQLTGRKRSKNSVY-----DS 319
OY 123 HDGSEFKSPDT--VCLSRGL-----LVKKAIDHDFIPSNLSILNALSGVAILHID 173
DB 320 SNKSDIESANTELKQALAKANADKVOADNLAKSIKEO-----LNNVSNNANTLSAKLTQKD 375
OY 174 DIRRYIEQKKKELYL-LKSSSVVRDGGKRVGSGAQKRTGRLKRPVKVEDMQLYRPF 232
DB 376 NT--TQQKTELEKEVQADQATKSNMTASQMSAKSSIDAKVAF----- 417
OY 233 YLQLTNMPFINYSIQPCSPFDVCKPSSMOKOTQYKRLIQ-----TDGDKYGTSIQLQ 286
DB 418 -----IKRKLETFPKQKKAFFNELKQTRNQIQEETITNNKNPNPNSSELISQLT 464

```

Fri Dec 28 08:22:43 2001

us-09-830-647-1.rpt

Page 10

```
OY 287 LKREKKKGYCECLOAYEDLETHLLSEOHNFPAOSNOYOVDIVSKLVFPVVEKOTP 346
DB 465 SKRDSKNSYTD--SNKSDIES-ANTELKQALAKANADKVOADNLAKSI-----510
OY 347 KKKRIKYSVGLSPVSAVYKK--TEQKEVELQHSQKDCQEDDTYKEDNFLKETOE 404
DB 511 -KEOLNNSVSANANTLSAKLTJDKDNTIOAKTEL---EKEVQKADAIKSN--TAS 560
OY 405 TEKRLFISEPIPHPSNELRGLENKMSKCSMLSTAEEDIRQNTOLPLAKKQECJLDI 464
DB 561 MOSAKSWLDKVAEITKLETFNKDKREKFNELKQTRNOIOEFINTKNPNYSSELISOL 620
OY 465 SEHTLSENDELELRVDHYKCNIOASVHVSDFSTDNS-----GSQPRKQSDTVLFPK 516
DB 621 TSKRDSKNSYTD-----SSNKSDIESANTELKQALAKANADKVOADNL--AK 665
OY 517 DLKREDLHSIFTHDGLITINSQEHLTVOAKAPFHPPEEPNEC-DFKAMDLSPSGK--573
DB 666 SIKEO-LNNSVSANANTLSAKLTJDKDNTIOAKTELEKEVQKANOAIKSNNTASQSAKSS 724
OY 574 IHRKYKIIIGNRKENLEPNAEFD--KRT-----EFTTOEENRICSSPVQOSLLDLQTSSE 626
DB 725 LDQKVAEITKLETFNKDKREKFNELKQTRNOIOEFINTKN--NPVYSELISOLTSK 780
OY 627 EKSEPLGFTSYTERKSGICNVLDIWEENSND 656
DB 781 RDSK---NSYTDSS--NKSDI-ESANTE 802
```

Search completed: December 27, 2001, 16:55:40  
Job time: 240 sec